

SEQUENCE LISTING

<110> Li, Yi
Ruben, Steven M.

<120> Human G-Protein Coupled Receptors

<130> 1488.1220001

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<150> 08/852,824

<151> 1997-05-07

<160> 18

<170> PatentIn Ver. 2.0

<210> 1

<211> 2247

<212> DNA

<213> genomic

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<221> CDS

<222> (226)..(1251)

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ttaaaaaggaa aataccagat gccactctgc aggctgcaat aactactact tactggatac 180

attcaaacc tccagaatca acagtttatca ggtaaccaac aagaa atg caa gcc gtc 237

Met Gln Ala Val

1

gac aat ctc acc tct gcg cct ggg aac acc agt ctg tgc acc aga gac 285
Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg Asp

5

10

15

20

tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc ctg ttt 333
Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu Phe
25 30 35

ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc ttt caa 381
Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe Gln
40 45 50

atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca gtc att 429
Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val Ile
55 60 65

tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt agt gat 477
Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu Ser Asp
70 75 80

gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa gtt acc 525
Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln Val Thr
85 90 95 100

tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc ctg gga 573
Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe Leu Gly
105 110 115

ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt aaa aca 621
Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe Lys Thr
120 125 130

tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt gtc atc 669
Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val Val Ile
135 140 145

tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg acc aac 717
Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu Thr Asn
150 155 160

agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt aaa tca 765
Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu Lys Ser
165 170 175 180

gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt caa gtc 813

Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys Gln Val
185 190 195

att ttc tgg att aat ttc tta att gtt att gta tgt tat aca ctc att 861
Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr Leu Ile
200 205 210

aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta ggt aaa 909
Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val Gly Lys
215 220 225

gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att gct gta 957
Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ile Ala Val
230 235 240

ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct tac acc 1005
Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro Tyr Thr
245 250 255 260

ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat act ctg 1053
Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn Thr Leu
265 270 275

ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat gca tgc 1101
Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn Ala Cys
280 285 290

ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga aat tcc 1149
Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg Asn Ser
295 300 305

ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg tcc cag 1197
Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu Ser Gln
310 315 320

gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa gag act 1245
Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu Glu Thr
325 330 335 340

cca atg taaaacaaatt aactaaggaa atatttcaat ctctttgtgt tcagaactcg 1301
Pro Met

ttaaagcaaa gcgctaagta aaaatattaa ctgacgaaga agcaactaag ttaataataa 1361

tgactctaaa gaaacagaag attacaaaag caatttcat ttaccttcc agtatgaaaa 1421

gctatcttaa aatatagaaa actaatctaa actgttagctg tattagcagc aaaacaaacg 1481

acatccaatt gtcatgctgc atgcaaaact acacagaatt catgtttgg cagagtttg 1541

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acttataaaa atttaagtaa gtgggataca caaagaataa taactattaa ctttcatta 1781

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gaagtcatta aaataaggag acttacttt atgacattct aatactaaaa aatatagaaa 1961

tatccctta attctagaga aactagttt actaatttt tacaacttca ataataccat 2021

cactgacact taccttattt aattagcttc tagaaaatag ctgctaatta ggttaatgaa 2081

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acaaatttac attaaactct aaatcattaa aaaaaaaaaa aaaaaa 2248

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<213> genomic

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Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg			
35	40	45	
Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys			
50	55	60	
Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys			
65	70	75	80
Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val			
85	90	95	
Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile			
100	105	110	
Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg			
115	120	125	
Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu			
130	135	140	
Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met			
145	150	155	160
Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser			
165	170	175	
Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr			
180	185	190	
Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys			
195	200	205	
Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg			
210	215	220	

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
305 310 315 320

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325 330 335

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<222> (50)..(1201)

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Thr Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu Ala Ala Gly

5

10

15

ggg cac agc cgg ctc att gtt ctg cac tac aac cac tac tcg ggc cgg ctg 154
Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser Gly Arg Leu

20 25 30 35

gcc ggg cgc ggg ggg ccg gag gat ggc ggc ctg ggg gcc ctg cgg ggg 202
Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala Leu Arg Gly
40 45 50

ctg tcg gtg gcc gcc agc tgc ctg gtg ctg gag aac ttg ctg gtg 250
Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn Leu Leu Val
55 60 65

ctg gcg gcc atc acc agc cac atg cgg tcg caa cgc tgg gtc tac tat 298
Leu Ala Ala Ile Thr Ser His Met Arg Ser Gln Arg Trp Val Tyr Tyr
70 75 80

tgc ctg gtg aac att acg atg agt gac ctg ctc acg ggc gcg gcc tac 346
Cys Leu Val Asn Ile Thr Met Ser Asp Leu Leu Thr Gly Ala Ala Tyr
85 90 95

ctg gcc aac gtg ctg ctg tcg ggg gcc cgc acc ttc cgt ctg gcg ccc 394
Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg Leu Ala Pro
100 105 110 115

gcc cag tgg ttc cta cgg aag ggc ctg ctc ttc acc gcc ctg gcc gcc 442
Ala Gln Trp Phe Leu Arg Lys Gly Leu Leu Phe Thr Ala Leu Ala Ala
120 125 130

tcc acc ttc agc ctg ctc ttc act gca ggg ttg cgc ttt gcc acc atg 490
Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Leu Arg Phe Ala Thr Met
135 140 145

gtg cgg ccg gtg gcc gag agc ggg gcc acc aag acc agc cgc gtc tac 538
Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser Arg Val Tyr
150 155 160

ggc ttc atc ggc ctc tgc tgg ctg ctg gcc gcg ctg ctg ggg atg ctg 586
Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu Gly Met Leu
165 170 175

cct ttg ctg ggc tgg aac tgc ctg tgc gcc ttt gac cgc tgc tcc agc 634
Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg Cys Ser Ser
180 185 190 195

ctt ctg ccc ctc tac tcc aag cgc tac atc ctc ttc tgc ctg gtg atc 682
Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys Leu Val Ile
200 205 210

ttc gcc ggc gtc ctg gcc acc atc atg ggc ctc tat ggg gcc atc ttc 730
Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly Ala Ile Phe
215 220 225

cgc ctg gtg cag gcc agc ggg cag aag gcc cca cgc cca gcg gcc cgc 778
Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro Ala Ala Arg
230 235 240

cgc aag gcc cgc cgc ctg ctg aag acg gtg ctg atg atc ctg ctg gcc 826
Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile Leu Ala
245 250 255

ttc ttg gtg tgc tgg gga cca ctc ttc ggg ctg ctg ctg gcc gac gtc 874
Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Ala Asp Val
260 265 270 275

ttt ggc tcc aac ctc tgg gcc cag gag tac ctg cgg ggc atg gac tgg 922
Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly Met Asp Trp
280 285 290

atc ctg gcc ctg gcc gtc ctc aac tcg gcg gtc aac ccc atc atc tac 970
Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro Ile Ile Tyr
295 300 305

tcc ttc cgc agc agg gag gtg tgc aga gcc gtg ctc agc ttc ctc tgc 1018
Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser Phe Leu Cys
310 315 320

tgc ggg tgt ctc cgg ctg ggc atg cga ggg ccc ggg gac tgc ctg gcc 1066
Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp Cys Leu Ala
325 330 335

cgg gcc gtc gag gct cac tcc gga gct tcc acc acc gac agc tct ctg 1114
Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp Ser Ser Leu
340 345 350 355

agg cca agg gac agc ttt cgc ggc tcc cgc tcg ctc agc ttt cg^g atg 1162
Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser Phe Arg Met
360 365 370

cg^g gag ccc ctg tcc agc atc tcc agc gtg cg^g agc atc tgaagttgca 1211
Arg Glu Pro Leu Ser Ser Ile Ser Val Arg Ser Ile
375 380

gtcttgcgtg tggatggtgc aaccaccggg tg^{cgt}gccag gcaggccctc ctggggtaca 1271

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ccctctctg ggcctcagta gggctcc^{ca} gctgcaaggg gtggactgtg ggatgc^{at}gc 1571

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35 40 45

Leu Arg Gly Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn
50 55 60

Leu Leu Val Leu Ala Ala Ile Thr Ser His Met Arg Ser Gln Arg Trp
65 70 75 80

Val Tyr Tyr Cys Leu Val Asn Ile Thr Met Ser Asp Leu Leu Thr Gly
85 90 95

Ala Ala Tyr Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg
100 105 110

Leu Ala Pro Ala Gln Trp Phe Leu Arg Lys Gly Leu Leu Phe Thr Ala
115 120 125

Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Leu Arg Phe
130 135 140

Ala Thr Met Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser
145 150 155 160

Arg Val Tyr Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu
165 170 175

Gly Met Leu Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg
180 185 190

Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys
195 200 205

Leu Val Ile Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly
210 215 220

Ala Ile Phe Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro
225 230 235 240

Ala Ala Arg Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile
245 250 255

Leu Leu Ala Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu
260 265 270

Ala Asp Val Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly
275 280 285

Met Asp Trp Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro
290 295 300

Ile Ile Tyr Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser
305 310 315 320

Phe Leu Cys Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp
325 330 335

Cys Leu Ala Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp
340 345 350

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Phe Arg Met Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg Ser Ile
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<212> DNA

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<212> DNA

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<212> DNA

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35 40 45

Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn Ser Thr Thr
50 55 60

Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe Thr Thr Ala
65 70 75 80

Leu Pro Thr Arg Ile Ala Tyr Tyr Ala Met Gly Phe Asp Trp Arg Ile
85 90 95

Gly Asp Ala Leu Cys Arg Ile Thr Ala Leu Val Phe Tyr Ile Asn Thr
100 105 110

Tyr Ala Gly Val Asn Phe Met Thr Cys Leu Ser Ile Asp Arg Phe Ile
115 120 125

Ala Val Val His Pro Leu Arg Tyr Asn Lys Ile Lys Arg Ile Glu His
130 135 140

Ala Lys Gly Val Cys Ile Phe Val Trp Ile Leu Val Phe Ala Gln Thr
145 150 155 160

Leu Pro Leu Leu Ile Asn Pro Met Ser Lys Gln Glu Ala Glu Arg Ile
165 170 175

Thr Cys Met Glu Tyr Pro Asn Phe Glu Glu Thr Lys Ser Leu Pro Trp
180 185 190

Ile Leu Leu Gly Ala Cys Phe Ile Gly Tyr Val Leu Pro Leu Ile Ile
195 200 205

Ile Lys Ile Cys Tyr Ser Gln Ile Cys Cys Lys Leu Phe Arg Thr Ala
210 215 220

Lys Gln Asn Pro Leu Thr Glu Lys Ser Gly Val Asn Lys Lys Ala Leu
225 230 235 240

Asn Thr Ile Ile Leu Ile Ile Val Val Phe Val Leu Cys Phe Thr Pro
245 250 255

Tyr His Val Ala Ile Ile Gln His Met Ile Lys Lys Leu Arg Phe Ser
260 265 270

Asn Phe Leu Glu Cys Ser Gln Arg His Ser Phe Gln Ile Ser Leu His
275 280 285

Phe Thr Val Cys Leu Met Asn Phe Asn Cys Cys Met Asp Pro Phe Ile
290 295 300

Tyr Phe Phe Ala Cys Lys Gly Tyr Lys Arg Lys Val Met Arg Met Leu
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25

30

Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr

35

40

45

Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile

50

55

60

Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met

65

70

75

80

Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val

85

90

95

Ala Tyr Thr Ala Asn Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu

100

105

110

Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu

115

120

125

Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile

130

135

140

Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu

145

150

155

160

Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly

165

170

175

Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser
180 185 190

Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr
195 200 205

Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile
210 215 220

Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn
225 230 235 240

Ile Ser Lys Ala Ser Arg Ser Ser Glu Asn Val Ala Leu Leu Lys Thr
245 250 255

Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu Phe
260 265 270

Ile Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp Ile
275 280 285

Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser Gly
290 295 300

Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg Ala
305 310 315 320

Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser Ala
325 330 335

Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg Ser
340 345 350

Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn Pro
355 360 365

Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
370 375 380